

WO 01/18047

PCT/AU00/01083

1/19

SEQUENCE LISTING

<110> The Council of the Queensland Institute of Medical Research

5

<120> Dendritic cell membrane FIRE

<160> 23

10

<170> PatentIn Ver. 2.1

<210> 1

<211> 681

15

<212> PRT

<213> Mus musculus

<400> 1

20

Met Gly Ser Arg Cys Leu Leu His Ala Ser Val Pro Gly Met Leu Leu  
1 5 10 15

Ile Trp Ser Ile Leu Gln Met Met Asn Ile Ser Ala Ser Cys Pro Gln  
20 25 30

25

Cys Asn Glu Asn Ala Ser Cys Phe Asn Ser Thr His Cys Val Cys Lys  
35 40 45

Glu Gly Phe Trp Thr Gly Ser Glu Asn Arg Arg Ile Ile Glu Pro His  
50 55 60

30

Glu Lys Cys Gln Asp Ile Asn Glu Cys Leu Leu Lys Glu Leu Val Cys  
65 70 75 80

35

Lys Asp Val Ser Tyr Cys Arg Asn Lys Ile Gly Thr Tyr Ile Cys Ser  
85 90 95

Cys Val Val Lys Tyr Pro Leu Phe Asn Trp Val Ala Gly Ile Ile Asn  
100 105 110

40

Ile Asp His Pro Asp Cys Tyr Val Asn Lys Ser Lys Asn Thr Gly Ser  
115 120 125

Lys Thr His Thr Leu Gly Val Leu Ser Glu Phe Lys Ser Lys Glu Glu  
130 135 140

45

Val Ala Lys Gly Ala Thr Lys Leu Leu Arg Lys Val Glu His His Ile  
145 150 155 160

50

Leu Asn Glu Asn Ser Asp Ile Pro Lys Lys Asp Glu Asn Pro Leu Leu  
165 170 175

Asp Ile Val Tyr Glu Thr Lys Arg Cys Lys Thr Met Thr Leu Leu Glu  
180 185 190

55

Ala Gly Asn Asn Thr Met Lys Val Asp Cys Thr Ser Gly Phe Lys Glu  
195 200 205

His Asn Ser Gly Gly Glu Thr Ala Val Ala Phe Ile Ala Tyr Lys Ser

WO 01/18047

PCT/AU00/01083

2/19

	210	215	220
	Leu Gly Asn Leu Leu Asn Gly Ser Phe Phe Ser Asn Glu Glu Gly Phe	225	230 235 240
5	Gln Glu Val Thr Leu Asn Ser His Ile Val Ser Gly Ala Ile Arg Ser	245	250 255
10	Glu Val Lys Pro Val Leu Ser Glu Pro Val Leu Leu Thr Leu Gln Asn	260	265 270
	Ile Gln Pro Ile Asp Ser Arg Ala Glu His Leu Cys Val His Trp Glu	275	280 285
15	Gly Ser Glu Glu Gly Gly Ser Trp Ser Thr Lys Gly Cys Ser His Val	290	295 300
	Tyr Thr Asn Asn Ser Tyr Thr Ile Cys Lys Cys Phe His Leu Ser Ser	305	310 315 320
20	Phe Ala Val Leu Met Ala Leu Pro His Glu Glu Asp Gly Val Leu Ser	325	330 335
	Ala Leu Ser Val Ile Thr Tyr Val Gly Leu Ser Leu Ser Leu Leu Cys	340	345 350
25	Leu Phe Leu Ala Ala Ile Thr Phe Leu Leu Cys Arg Pro Ile Gln Asn	355	360 365
30	Thr Ser Thr Thr Leu His Leu Gln Leu Ser Ile Cys Leu Phe Leu Ala	370	375 380
	Asp Leu Leu Phe Leu Thr Gly Ile Asn Arg Thr Lys Pro Lys Val Leu	385	390 395 400
35	Cys Ser Ile Ile Ala Gly Met Leu His Tyr Leu Tyr Leu Ala Ser Phe	405	410 415
	Met Trp Met Phe Leu Glu Gly Leu His Leu Phe Leu Thr Val Ser Asn	420	425 430
40	Leu Lys Val Ala Asn Tyr Ser Asn Ser Gly Arg Phe Lys Lys Arg Phe	435	440 445
	Met Tyr Pro Val Gly Tyr Gly Leu Pro Ala Phe Ile Val Ala Val Ser	450	455 460
45	Ala Ile Ala Gly His Lys Asn Tyr Gly Thr His Asn His Cys Trp Leu	465	470 475 480
50	Ser Leu His Arg Gly Phe Ile Trp Ser Phe Leu Gly Pro Ala Ala Ala	485	490 495
	Ile Ile Leu Ile Asn Leu Val Phe Tyr Phe Leu Ile Ile Trp Ile Leu	500	505 510
55	Arg Ser Lys Leu Ser Ser Leu Asn Lys Glu Val Ser Thr Leu Gln Asp	515	520 525

WO 01/18047

PCT/AU00/01083

3/19

Thr Lys Val Met Thr Phe Lys Ala Ile Val Gln Leu Phe Val Leu Gly  
530 535 540

5 Cys Ser Trp Gly Ile Gly Leu Phe Ile Phe Ile Glu Val Gly Lys Thr  
545 550 555 560

Val Arg Leu Ile Val Ala Tyr Leu Phe Thr Ile Ile Asn Val Leu Gln  
565 570 575

10 Gly Val Leu Ile Phe Met Val His Cys Leu Leu Asn Arg Gln Val Arg  
580 585 590

15 Met Glu Tyr Lys Lys Trp Phe His Arg Leu Arg Lys Glu Val Glu Ser  
595 600 605

Glu Ser Thr Glu Val Ser His Ser Thr Thr His Thr Lys Met Gly Leu  
610 615 620

20 Ser Leu Asn Leu Glu Asn Phe Cys Pro Thr Gly Asn Leu His Asp Pro  
625 630 635 640

Ser Asp Ser Ile Leu Pro Ser Thr Glu Val Ala Gly Val Tyr Leu Ser  
645 650 655

25 Thr Pro Arg Ser His Met Gly Ala Glu Asp Val Asn Ser Gly Thr His  
660 665 670

30 Ala Tyr Trp Ser Arg Thr Ile Ser Asp  
675 680

<210> 2  
<211> 635  
35 <212> PRT  
<213> Homo sapiens

<400> 2  
40 Ala Ser Cys Pro Pro Cys Pro Lys Tyr Ala Ser Cys His Asn Ser Thr  
1 5 10 15

His Cys Thr Cys Glu Asp Gly Phe Arg Ala Arg Ser Gly Arg Thr Tyr  
20 25 30

45 Phe His Asp Ser Ser Glu Lys Cys Glu Asp Ile Asn Glu Cys Glu Thr  
35 40 45

Gly Leu Ala Lys Cys Lys Tyr Lys Ala Tyr Cys Arg Asn Lys Val Gly  
50 55 60

50 Gly Tyr Ile Cys Ser Cys Leu Val Lys Tyr Thr Leu Phe Asn Phe Leu  
65 70 75 80

Ala Gly Ile Ile Asp Tyr Asp His Pro Asp Cys Tyr Glu Asn Asn Ser  
85 90 95

55 Gln Gly Thr Thr Gln Ser Asn Val Asp Ile Trp Glu Asn Leu Arg Arg  
100 105 110

WO 01/18047

PCT/AU00/01083

4/19

	Asn	Gly	Ser	Arg	Glu	Asp	Phe	Ala	Arg	Arg	Ala	Thr	Gln	Leu	Ile	Gln	
							115				120			125			
5	Ser	Val	Glu	Leu	Ser	Ile	Trp	Asn	Ala	Ser	Phe	Ala	Ser	Pro	Gly	Lys	
		130					135					140					
	Gly	Gln	Ile	Ser	Glu	Phe	Asp	Ile	Val	Tyr	Glu	Thr	Lys	Arg	Cys	Asn	
	145					150					155				160		
10	Glu	Thr	Arg	Glu	Asn	Ala	Phe	Leu	Glu	Ala	Gly	Asn	Asn	Thr	Met	Asp	
					165					170					175		
	Ile	Asn	Cys	Ala	Asp	Ala	Leu	Lys	Gly	Asn	Leu	Arg	Glu	Ser	Thr	Ala	
15				180					185					190			
	Val	Ala	Leu	Ile	Thr	Tyr	Gln	Ser	Leu	Gly	Asp	Ile	Leu	Asn	Ala	Ser	
		195					200						205				
20	Phe	Phe	Ser	Lys	Arg	Lys	Gly	Met	Gln	Glu	Val	Lys	Leu	Asn	Ser	Tyr	
	210						215					220					
	Val	Val	Ser	Gly	Thr	Val	Gly	Leu	Lys	Glu	Lys	Ile	Ser	Leu	Ser	Glu	
	225					230					235					240	
25	Pro	Val	Phe	Leu	Thr	Phe	Arg	His	Asn	Gln	Pro	Gly	Asp	Lys	Arg	Thr	
					245					250					255		
	Lys	His	Ile	Cys	Val	Tyr	Trp	Glu	Gly	Ser	Glu	Gly	Gly	Arg	Trp	Ser	
30				260					265					270			
	Thr	Glu	Gly	Cys	Ser	His	Val	His	Ser	Asn	Gly	Ser	Tyr	Thr	Lys	Cys	
			275					280					285				
35	Lys	Cys	Phe	His	Leu	Ser	Ser	Phe	Ala	Val	Leu	Val	Ala	Leu	Ala	Pro	
		290					295					300					
	Lys	Glu	Asp	Pro	Val	Leu	Thr	Val	Ile	Thr	Gln	Val	Gly	Leu	Thr	Ile	
	305					310					315				320		
40	Ser	Leu	Leu	Cys	Leu	Phe	Leu	Ala	Ile	Leu	Thr	Phe	Leu	Leu	Cys	Arg	
				325						330					335		
	Pro	Ile	Gln	Asn	Thr	Ser	Thr	Ser	Leu	His	Leu	Glu	Leu	Ser	Leu	Cys	
45				340					345					350			
	Leu	Phe	Leu	Ala	His	Leu	Leu	Phe	Leu	Thr	Gly	Ile	Asn	Arg	Thr	Glu	
		355					360					365					
50	Pro	Glu	Val	Leu	Cys	Ser	Ile	Ile	Ala	Gly	Leu	Leu	His	Phe	Leu	Tyr	
		370					375					380					
	Leu	Ala	Cys	Phe	Thr	Trp	Met	Leu	Leu	Glu	Gly	Leu	His	Leu	Phe	Leu	
	385					390					395				400		
55	Thr	Val	Arg	Asn	Leu	Lys	Val	Ala	Asn	Tyr	Thr	Ser	Thr	Gly	Arg	Phe	
				405						410					415		

WO 01/18047

PCT/AU00/01083

5/19

Lys Lys Arg Phe Met Tyr Pro Val Gly Tyr Gly Ile Pro Ala Val Ile  
 420 425 430  
 5 Ile Ala Val Ser Ala Ile Val Gly Pro Gln Asn Tyr Gly Thr Phe Thr  
 435 440 445  
 His Cys Trp Leu Lys Leu Asp Lys Gly Phe Ile Trp Ser Phe Met Gly  
 450 455 460  
 10 Pro Val Ala Val Ile Ile Leu Ile Asn Leu Val Phe Tyr Phe Gln Val  
 465 470 475 480  
 Leu Trp Ile Leu Arg Ser Lys Leu Ser Ser Leu Asn Lys Glu Val Ser  
 485 490 495  
 15 Thr Ile Gln Asp Thr Arg Val Met Thr Phe Lys Ala Ile Ser Gln Leu  
 500 505 510  
 Phe Ile Leu Gly Cys Ser Trp Gly Leu Gly Phe Phe Met Val Glu Glu  
 515 520 525  
 20 Val Gly Lys Thr Ile Gly Ser Ile Ile Ala Tyr Ser Phe Thr Ile Ile  
 530 535 540  
 25 Asn Thr Leu Gln Gly Val Leu Leu Phe Val Val His Cys Leu Leu Asn  
 545 550 555 560  
 Arg Gln Val Arg Met Glu Tyr Lys Lys Trp Phe Ser Gly Met Arg Lys  
 565 570 575  
 30 Gly Val Glu Thr Glu Ser Thr Glu Met Ser Arg Ser Thr Thr Gln Thr  
 580 585 590  
 Lys Thr Glu Glu Val Gly Lys Ser Ser Glu Ile Phe His Lys Gly Gly  
 595 600 605  
 35 Thr Ala Ser Ser Ser Ala Glu Ser Thr Lys Gln Pro Gln Pro Gln Val  
 610 615 620  
 40 His Leu Val Ser Ala Ala Trp Leu Lys Met Asn  
 625 630 635  
 45 <210> 3  
 <211> 3258  
 <212> DNA  
 <213> Mus musculus  
 <400> 3  
 50 accactgctt cattgctgct gagaatgttc caggctgagt gagaagtaaa aattcatcat 60  
 ctctgaagaa ctcttaacca gccctgttga agaaattccc agaattgtga tgggagcaac 120  
 tagagatatg ggaagcaggt gccctctgca tgcctcagtt cctggaatgc tgcttatctg 180  
 gtcaatatta caaatgatga atatttcagc ttcctgtccc cagtgcgaatg aaaatgccag 240  
 ctgcttcaac agcaccact ggtttgttaa agaaggattc tggacgggct ctgagaatag 300  
 aagaattatt gagcccatg agaaatgtca agatattaat gagtgtctac tgaaagaatt 360  
 55 ggtatgcaag gatgtgtcgt actgcagaaa taaaattggg acttacatat gcagctgtgt 420  
 agtaaaatat cctttgttca actgggtagc tggcattatt aatattgatc acctgattg 480  
 ttatgtgaac aagagcaaga atacaggatc aaaaacacat actttgggag tactgagtga 540  
 atttaaatcc aaagaggagg ttgcaaaagg agctaccaag ttacttcgca aagtgggaac 600

WO 01/18047

PCT/AU00/01083

6/19

	tcacatcttg	aatgaaaact	cagatatacc	aaaaaaggat	gaaaatcctt	tattggatat	660
	agtgtatgaa	actaagagggt	gcaagacgat	gactcttcta	gaagctggca	acaacacaat	720
	gaaggttgac	tgcactagtg	gtttcaaaaga	gcacaacagt	ggaggtgaaa	ctgcagtggc	780
	tttcattgca	tataagtcct	ttgggaatct	tctaaatggg	tcctttttta	gtaatgaaga	840
5	aggggttcag	gaagtgcac	tgaactctca	catcgtagt	ggagccattc	gtcagagggt	900
	caaacctgtc	ctctctgaac	ctgtactcct	gactttacaa	aatattcagc	ccattgactc	960
	aagagcagaa	catctctgtg	tccattggga	aggatcagag	gaagggggga	gtcggcttac	1020
	caaaggatgc	tctcacgtgt	acaaccaataa	ttcctacacc	atttgcaagt	gtttccacct	1080
	gtccagcttt	gctgtgctca	tggctctacc	ccatgaggag	gatggtgtgc	tttctgcact	1140
10	ctctgtgac	acctatgtgg	gactgagtcct	ttctctcttg	tgctatttcc	tggcgcccat	1200
	cacttttctc	ctgtgcccac	ccattcagaa	taccagcacg	acactccacc	tcagctcttc	1260
	catctgcctt	ttcctggctg	acctctctct	cctcacaggc	atcaacagaa	ctaagcctaa	1320
	ggtgctgtgc	tccatcatag	cggggtatgtt	gcactaacctc	tacttggtct	ccttcactgt	1380
	gatgtttctg	gaagggctac	atctttttct	cactgtgagc	aatctcaaaag	tggccaacta	1440
15	cagcaactca	ggcagattca	agaagagggtt	catgtatcct	gtaggatatg	ggcttctctg	1500
	ttttattggt	gctgtatctg	caatagctgg	ccacaagaat	tatggaacac	acaaccactg	1560
	ctggctcagc	cttcacagag	gattcatctg	gagcttcttg	gggcccagcg	cagccattat	1620
	ctcgataaac	ctgggtgtct	acttctctaat	aatatggatt	ttgagaagca	aatcttcttc	1680
	tctcaataaaa	gaagtttcta	cacttcaaga	cacaaagggt	atgacattta	aagccattgt	1740
20	ccagttattt	gtggtgggat	gttcttgggg	cattggcttg	tttattttca	ttgaagttgg	1800
	gaagacagtg	agactgatcg	ttgcttatct	gttcaccatc	atcaatgtcc	tcaggggtgt	1860
	tttgatattt	atggtacatt	gtctgcttaa	tcgccagggtg	cggatggaaat	ataagaagtg	1920
	gtttcataga	ctgcgggaag	aagttgaaaag	tgaaaagcact	gaagtgtctc	attctactac	1980
	tcacacaaaa	atgggtcttt	ctctgaacct	ggaaaatttc	tgcccaacag	gaaacctcca	2040
25	tgatccctct	gactccatcc	ttccaagtac	tgaagtagca	ggtgtatatc	taagcacacc	2100
	caggtctcac	atgggtgctg	aggatgtgaa	ctcaggtact	cacgcttact	ggagcagaac	2160
	tattagtgat	tgaatcagct	ccttccccca	agcctcttac	agtacatttt	aatctgtact	2220
	gtgccatgca	catgaagcta	taattgtctag	tctggtaaaa	caactgttgc	atattccatg	2280
30	atcatttcat	tttatctcta	cttgcaaaaag	ttagccttct	tttatatca	tttctatttc	2340
	tctttctttt	gtttatatat	agcttccagtt	gagtgggttt	ctagtcttaa	tgttctagat	2400
	cactattttt	ttttcagtha	acctttattg	gtattttagt	cctgtgtagt	gtataccact	2460
	ggaatatttt	tatttcttta	attttgaggt	taaaactatg	ttacatcatt	tttctttttt	2520
	ttctttccca	caatccctct	gtatactttt	ttcctggtgt	ctattttatt	gttctctacat	2580
	gcataatatat	tttatgcaaa	acataatatat	gtataaatat	aaatatatat	tcttatatgc	2640
35	atgaaaaacca	tctacttcat	ccaataaatg	ttccttctat	gtatgttttc	aggacaggga	2700
	caacaatagc	tatggtagca	tgccaggggga	aagccacacag	gacccagcc	ttatacaaaag	2760
	aatcagaggc	aactgaggag	tgctgagttg	aagggaattgt	cttaccacag	ggaggggcaca	2820
	ttaattgggt	atctaataca	aaatgttcag	ccccaaaaact	gttaagataa	aagccatata	2880
	gcactcttagg	aagtatctac	cctgatacac	cctttattgga	atatcatcca	catgtttatt	2940
40	gtgtgttctg	aagagggtct	gttgaaatttc	taagggttga	tcagtttaat	tgtgccattt	3000
	tatattccag	gtgtttggct	ttgtctgagt	gaataatgct	atatttccct	gtatgtgtca	3060
	tctttgactg	ttattttttc	ctggcgatac	tttattcaac	aagaacctag	agccttggtt	3120
	tattactttt	tcttccatag	aaaactatatt	tgtcttccag	gattagatat	gatcaatatt	3180
	tcttatatgc	atgtatcaaa	tatcatgatg	aaatatatta	ctgtgcataa	ttaataactg	3240
45	gcaataaagt	ccaaggga					3258

<210> 4  
 <211> 2798  
 50 <212> DNA  
 <213> Homo sapiens

	<400> 4					
55	gttctctgtc	ctccatgccc	taaatatgcc	agctgccaca	acagcaccca	ctgtacttgt
	gaagatggct	ttcgggccag	gtctggcagg	acataacttc	atgattccctc	tgagaagtgt
	gaagatatta	atgaatgtga	aactgggctg	gcaaagtgc	agtataaagc	atattgtagg
	aataaagttg	gaggttacat	ctgtagctgt	ttggtaaaat	atactttatt	caacttctctg
	gctggatatta	tagattatga	tcatccggat	tgctacgaga	acaatagtca	agggacgaca
						300

WO 01/13047

PCT/AU00/01083

7/19

```

cagtcaaacg tggatatttg ggaaaatcty agaagaaatg gaagcagaga ggacttttgc 360
agaaggggcta ctcaactaat tcaaagcgtg gagtttgaca tctggaatgc gagtttttgc 420
tctccaggaa aggggtcaaat ttctggaattt gatatagtct atgaaaccaaa gaggttgcaat 480
gagacaaggg agaattgcttt tctggaagct ggaaataaca ccatggatat caactgtgct 540
5 gatgctttta aaggaaacct aagagagagc actgcagttg ccctaatacac ttatcaatct 600
cttgggggata ttctgaatgc atcctttttt agtaaacgaa aagggatgca ggaagtaaaa 660
ctgaactcctt acgtttgtgag cggcacccgtc gglttgaggg aaaaaatttc cctctctgaa 720
cctgtgtctcc tgacttttctg ccataatcag cctygtgaca agagaacaaa acatatctgt 780
gtctactggg agggatcaga gggaggccgc tgggtccacgg agggctgtct tcatgtgcac 840
10 agcaacgggt cttacaccaa atgcaagtgc ttccatctgt ccagctttgc cgtcctcgtg 900
gctcttgccc ccaaggagga cctgtgtcty accgtgatca cccagggtggg gctgaccatc 960
teyctgctgt gctcttctct ggccatcctc accttctctc tgtgcccggc catccagaac 1020
accagcaect cctctcatct agagctctct cctgtgctct tcttgcccca cctctgttc 1080
ctgacgggca tcaacagaa tgagcctgag gtgctgtgct ccatcattgc agggctgtct 1140
15 cacttctctt acctggtctt cttcacctgg atgctctctg aagggctgca cctcttctct 1200
accgtcagga acctcaaggg ggccaactac accagcaggg gcagattcaa gaagagggtc 1260
atgtaccctg taggtacgg gatccagct ggtattattg ctgtgtcagc aatagtggga 1320
ccccagaatt atggaacatb tactcactgt tggctcaagg ttgataaagg attcatctgg 1380
agcttcatgg ggccagtagc agtctattatc ttgataaacc tgggtgttcta cttccaagtt 1440
20 ctgtgggatt tgagaagcaa actttctctc ctcaataaag aagtttccac cattcaggac 1500
accagagtcga tgacatttaa agcctatttct cagctattta tcttggtgtg ttcttggggc 1560
cttgggtttt ttatggttga agagtaggg aagacgattg gatcaatcat tgcatactca 1620
ttcaccatca tcaacacctc tcaaggagtg ttgctctttg tggtagactg tctctttaat 1680
cgccagggttc gaatggaata taalaaagtg ttttagtggg tgccgaaagg ggtagaaact 1740
25 gaaagcactg agatgtctcg ctctactacc caaaccaaaa cggagaaggt ggggaagtcc 1800
tcagaaatct ttcataaagg aggcactgca tcatcatcty cagagtcaac caagcaaccg 1860
cagccacagg ttcatctcgt cctgtctgct tggctaaaga tgaaactgacc tggcaagtgc 1920
catggcaatg acccggaagt taccgtctct ttccgtttgt ctacagegcc cctgtgggtc 1980
30 cacatagatt ggacaaatgc cactatttct agotttctct tgaaaagtct aggtcattc 2040
acctattttg gctttttatg ttcatagaaa gaacaagaca tttgggagaa ttcttagatc 2100
cagagtccag tagtgtggca cgtgcaatga agtgtcgga ggatgcattt taaagatggt 2160
ggcggggaga agtggatttt tctctttgca gctactgcca ccttgccaga aactcacta 2220
actggcctct ggrrattcagc tcatagtctc ctttctggcc tctctgtctg attttatgct 2280
ccccaaagatc ttacattaac actccacatt cacataatcc aacaattttc atatggatca 2340
35 gtartaaaga ggggtgttgc ttttgcaata caaaaatgca ttatcagggt ctggagagga 2400
tgtggagaaa taggaacact tttaactgtg tgggtgggact gtaaaactagt tcaaccatcg 2460
tggaagtccag tgtggcgatt cctcagggat ctagaactag aaataccatt tgacacagct 2520
atcccattac tgggtatata cccaaggac tataaatcat gctgctataa agacacatgc 2580
acacgtatgt ttattgtggc attattcaca atagcaaaga cttggaacca acccaatgt 2640
40 ccaacaatga tagactggat taagaaaatg tggcacatat acaccatgga atactatgca 2700
gccataaaaa atgatygatt catgtccttt gtagggacat ggaatgaaatc cggaaattccg 2760
ccgatactga cgggtccag gagtctctgc caccaatc 2798

```

45 <210> 5  
<211> 886  
<212> PRT  
<213> Homo sapiens

50 <400> 5  
Met Arg Gly Phe Asn Leu Leu Leu Phe Trp Gly Cys Cys Val Met His  
1 5 10 15

55 Ser Trp Glu Gly His Ile Arg Pro Thr Arg Lys Pro Asn Thr Lys Gly  
20 25 30

Asn Asn Cys Arg Asp Ser Thr Leu Cys Pro Ala Tyr Ala Thr Cys Thr  
35 40 45

WO 01/18047

PCT/AU00/01083

8/19

	Asn	Thr	Val	Asp	Ser	Tyr	Tyr	Cys	Thr	Cys	Lys	Gln	Gly	Phe	Leu	Ser	
	50						55					60					
5	Ser	Asn	Gly	Gln	Asn	His	Phe	Lys	Asp	Pro	Gly	Val	Arg	Cys	Lys	Asp	
	65					70					75					80	
	Ile	Asp	Glu	Cys	Ser	Gln	Ser	Pro	Gln	Pro	Cys	Gly	Pro	Asn	Ser	Ser	
					85					90					95		
10	Cys	Lys	Asn	Leu	Ser	Gly	Arg	Tyr	Lys	Cys	Ser	Cys	Leu	Asp	Gly	Phe	
				100					105					110			
	Ser	Ser	Pro	Thr	Gly	Asn	Asp	Trp	Val	Pro	Gly	Lys	Pro	Gly	Asn	Phe	
15			115					120					125				
	Ser	Cys	Thr	Asp	Ile	Asn	Glu	Cys	Leu	Thr	Ser	Arg	Val	Cys	Pro	Glu	
		130					135					140					
20	His	Ser	Asp	Cys	Val	Asn	Ser	Met	Gly	Ser	Tyr	Ser	Cys	Ser	Cys	Gln	
	145					150					155					160	
	Val	Gly	Phe	Ile	Ser	Arg	Asn	Ser	Thr	Cys	Glu	Asp	Val	Asn	Glu	Cys	
				165						170					175		
25	Ala	Asp	Pro	Arg	Ala	Cys	Pro	Glu	His	Ala	Thr	Cys	Asn	Asn	Thr	Val	
				180					185					190			
	Gly	Asn	Tyr	Ser	Cys	Phe	Cys	Asn	Pro	Gly	Phe	Glu	Ser	Ser	Ser	Gly	
30			195					200					205				
	His	Leu	Ser	Cys	Gln	Gly	Leu	Lys	Ala	Ser	Cys	Glu	Asp	Ile	Asp	Glu	
		210					215					220					
35	Cys	Thr	Glu	Met	Cys	Pro	Ile	Asn	Ser	Thr	Cys	Thr	Asn	Thr	Pro	Gly	
	225					230					235					240	
	Ser	Tyr	Phe	Cys	Thr	Cys	His	Pro	Gly	Phe	Ala	Pro	Ser	Ser	Gly	Gln	
				245						250					255		
40	Leu	Asn	Phe	Thr	Asp	Gln	Gly	Val	Glu	Cys	Arg	Asp	Ile	Asp	Glu	Cys	
				260					265					270			
	Arg	Gln	Asp	Pro	Ser	Thr	Cys	Gly	Pro	Asn	Ser	Ile	Cys	Thr	Asn	Ala	
45			275					280					285				
	Leu	Gly	Ser	Tyr	Ser	Cys	Gly	Cys	Ile	Val	Gly	Phe	His	Pro	Asn	Pro	
		290					295					300					
50	Glu	Gly	Ser	Gln	Lys	Asp	Gly	Asn	Phe	Ser	Cys	Gln	Arg	Val	Leu	Phe	
	305					310					315					320	
	Lys	Cys	Lys	Glu	Asp	Val	Ile	Pro	Asp	Asn	Lys	Gln	Ile	Gln	Gln	Cys	
				325						330					335		
55	Gln	Glu	Gly	Thr	Ala	Val	Lys	Pro	Ala	Tyr	Val	Ser	Phe	Cys	Ala	Gln	
				340					345					350			





WO 01/18047

PCT/AU00/01083

10/19

	660	665	670
	His Tyr Leu Phe Leu Ala Cys	Phe Phe Trp Met Leu Val Glu Ala Val	
	675	680	685
5	Ile Leu Phe Leu Met Val Arg	Asn Leu Lys Val Val Asn Tyr Phe Ser	
	690	695	700
10	Ser Arg Asn Ile Lys Met Leu His Ile Cys Ala Phe Gly Tyr Gly Leu		
	705	710	715
	Pro Met Leu Val Val Val Ile Ser Ala Ser Val Gln Pro Gln Gly Tyr		
	725	730	735
15	Gly Met His Asn Arg Cys Trp Leu Asn Thr Glu Thr Gly Phe Ile Trp		
	740	745	750
	Ser Phe Leu Gly Pro Val Cys Thr Val Ile Val Ile Asn Ser Leu Leu		
	755	760	765
20	Leu Thr Trp Thr Leu Trp Ile Leu Arg Gln Arg Leu Ser Ser Val Asn		
	770	775	780
25	Ala Glu Val Ser Thr Leu Lys Asp Thr Arg Leu Leu Thr Phe Lys Ala		
	785	790	795
	Phe Ala Gln Leu Phe Ile Leu Gly Cys Ser Trp Val Leu Gly Ile Phe		
	805	810	815
30	Gln Ile Gly Pro Val Ala Gly Val Met Ala Tyr Leu Phe Thr Ile Ile		
	820	825	830
	Asn Ser Leu Gln Gly Ala Phe Ile Phe Leu Ile His Cys Leu Leu Asn		
	835	840	845
35	Gly Gln Val Arg Glu Glu Tyr Lys Arg Trp Ile Thr Gly Lys Thr Lys		
	850	855	860
40	Pro Ser Ser Gln Ser Gln Thr Ser Arg Ile Leu Leu Ser Ser Met Pro		
	865	870	875
	Ser Ala Ser Lys Thr Gly		
	885		
45			
	<210> 6		
	<211> 931		
	<212> PRT		
	<213> Mus musculus		
50			
	<400> 6		
	Met Trp Gly Phe Trp Leu Leu Leu Phe Trp Gly Phe Ser Gly Met Tyr		
	1	5	10 15
55	Arg Trp Gly Met Thr Thr Leu Pro Thr Leu Gly Gln Thr Leu Gly Gly		
	20	25	30
	Val Asn Glu Cys Gln Asp Thr Thr Thr Cys Pro Ala Tyr Ala Thr Cys		

WO 01/18047

PCT/AU00/01083

11/19

	35	40	45
	Thr Asp Thr Thr Asp Ser Tyr Tyr Cys Thr Cys Lys Arg Gly Phe Leu		
5	50	55	60
	Ser Ser Asn Gly Gln Thr Asn Phe Gln Gly Pro Gly Val Glu Cys Gln		
	65	70	75
10	Asp Val Asn Glu Cys Leu Gln Ser Asp Ser Pro Cys Gly Pro Asn Ser		
	85	90	95
	Val Cys Thr Asn Ile Leu Gly Arg Ala Lys Cys Ser Cys Leu Arg Gly		
	100	105	110
15	Phe Ser Ser Ser Thr Gly Lys Asp Trp Ile Leu Gly Ser Leu Asp Asn		
	115	120	125
	Phe Leu Cys Ala Asp Val Asp Glu Cys Leu Thr Ile Gly Ile Cys Pro		
	130	135	140
20	Lys Tyr Ser Asn Cys Ser Asn Ser Val Gly Ser Tyr Ser Cys Thr Cys		
	145	150	155
	Gln Pro Gly Phe Val Leu Asn Gly Ser Ile Cys Glu Asp Glu Asp Glu		
	165	170	175
25	Cys Val Thr Arg Asp Val Cys Pro Glu His Ala Thr Cys His Asn Thr		
	180	185	190
30	Leu Gly Ser Tyr Tyr Cys Thr Cys Asn Ser Gly Leu Glu Ser Ser Gly		
	195	200	205
	Gly Gly Pro Met Phe Gln Gly Leu Asp Glu Ser Cys Glu Asp Val Asp		
	210	215	220
35	Glu Cys Ser Arg Asn Ser Thr Leu Cys Gly Pro Thr Phe Ile Cys Ile		
	225	230	235
	Asn Thr Leu Gly Ser Tyr Ser Cys Ser Cys Pro Ala Gly Phe Ser Leu		
	245	250	255
40	Pro Thr Phe Gln Ile Leu Gly His Pro Ala Asp Gly Asn Cys Thr Asp		
	260	265	270
45	Ile Asp Glu Cys Asp Asp Thr Cys Pro Leu Asn Ser Ser Cys Thr Asn		
	275	280	285
	Thr Ile Gly Ser Tyr Phe Cys Thr Cys His Pro Gly Phe Ala Ser Ser		
	290	295	300
50	Asn Gly Gln Leu Asn Phe Lys Asp Leu Glu Val Thr Cys Glu Asp Ile		
	305	310	315
	Asp Glu Cys Thr Gln Asp Pro Leu Gln Cys Gly Leu Asn Ser Val Cys		
	325	330	335
55	Thr Asn Val Pro Gly Ser Tyr Ile Cys Gly Cys Leu Pro Asp Phe Gln		
	340	345	350

WO 01/18047

PCT/AU00/01083

12/19

	Met	Asp	Pro	Glu	Gly	Ser	Gln	Gly	Tyr	Gly	Asn	Phe	Asn	Cys	Lys	Arg
			355					360					365			
5	Ile	Leu	Phe	Lys	Cys	Lys	Glu	Asp	Leu	Ile	Leu	Gln	Ser	Glu	Gln	Ile
	370						375					380				
	Gln	Gln	Cys	Gln	Ala	Val	Gln	Gly	Arg	Asp	Leu	Gly	Tyr	Ala	Ser	Phe
	385					390					395					400
10	Cys	Thr	Leu	Val	Asn	Ala	Thr	Phe	Thr	Ile	Leu	Asp	Asn	Thr	Cys	Glu
					405					410					415	
	Asn	Lys	Ser	Ala	Pro	Val	Ser	Leu	Gln	Ser	Ala	Ala	Thr	Ser	Val	Ser
15				420					425					430		
	Leu	Val	Leu	Glu	Gln	Ala	Thr	Thr	Trp	Phe	Glu	Leu	Ser	Lys	Glu	Glu
		435						440					445			
20	Thr	Ser	Thr	Leu	Gly	Thr	Ile	Leu	Leu	Glu	Thr	Val	Glu	Ser	Thr	Met
	450						455					460				
	Leu	Ala	Ala	Leu	Leu	Ile	Pro	Ser	Gly	Asn	Ala	Ser	Gln	Met	Ile	Gln
	465					470					475					480
25	Thr	Glu	Tyr	Leu	Asp	Ile	Glu	Ser	Lys	Val	Ile	Asn	Glu	Glu	Cys	Lys
				485						490					495	
	Glu	Asn	Glu	Ser	Ile	Asn	Leu	Ala	Ala	Arg	Gly	Asp	Lys	Met	Asn	Val
30				500					505					510		
	Gly	Cys	Phe	Ile	Ile	Lys	Glu	Ser	Val	Ser	Thr	Gly	Ala	Pro	Gly	Val
			515					520					525			
35	Ala	Phe	Val	Ser	Phe	Ala	His	Met	Glu	Ser	Val	Leu	Asn	Glu	Arg	Phe
	530						535					540				
	Phe	Glu	Asp	Gly	Gln	Ser	Phe	Arg	Lys	Leu	Arg	Met	Asn	Ser	Arg	Val
	545					550				555						560
40	Val	Gly	Gly	Thr	Val	Thr	Gly	Glu	Lys	Lys	Glu	Asp	Phe	Ser	Lys	Pro
				565						570					575	
	Ile	Ile	Tyr	Thr	Leu	Gln	His	Ile	Gln	Pro	Lys	Gln	Lys	Ser	Glu	Arg
45			580						585					590		
	Pro	Ile	Cys	Val	Ser	Trp	Asn	Thr	Asp	Val	Glu	Asp	Gly	Arg	Trp	Thr
		595					600						605			
50	Pro	Ser	Gly	Cys	Glu	Ile	Val	Glu	Ala	Ser	Glu	Thr	His	Thr	Val	Cys
	610						615					620				
	Ser	Cys	Asn	Arg	Met	Ala	Asn	Leu	Ala	Ile	Ile	Met	Ala	Ser	Gly	Glu
	625					630					635					640
55	Leu	Thr	Met	Glu	Phe	Ser	Leu	Tyr	Ile	Ile	Ser	His	Val	Gly	Thr	Val
					645					650					655	

WO 01/18047

PCT/AU00/01083

13/19

Ile Ser Leu Val Cys Leu Ala Leu Ala Ile Ala Thr Phe Leu Leu Cys  
 660 665 670  
 5 Arg Ala Val Gln Asn His Asn Thr Tyr Met His Leu His Leu Cys Val  
 675 680 685  
 Cys Leu Phe Leu Ala Lys Ile Leu Phe Leu Thr Gly Ile Asp Lys Thr  
 690 695 700  
 10 Asp Asn Gln Thr Ala Cys Ala Ile Ile Ala Gly Phe Leu His Tyr Leu  
 705 710 715 720  
 Phe Leu Ala Cys Phe Phe Trp Met Leu Val Glu Ala Val Met Leu Phe  
 725 730 735  
 15 Leu Met Val Arg Asn Leu Lys Val Val Asn Tyr Phe Ser Ser Arg Asn  
 740 745 750  
 Ile Lys Met Leu His Leu Cys Ala Phe Gly Tyr Gly Leu Pro Val Leu  
 755 760 765  
 20 Val Val Ile Ile Ser Ala Ser Val Gln Pro Arg Gly Tyr Gly Met His  
 770 775 780  
 25 Asn Arg Cys Trp Leu Asn Thr Glu Thr Gly Phe Ile Trp Ser Phe Leu  
 785 790 795 800  
 Gly Pro Val Cys Met Ile Ile Thr Ile Asn Ser Val Leu Leu Ala Trp  
 805 810 815  
 30 Thr Leu Trp Val Leu Arg Gln Lys Leu Cys Ser Val Ser Ser Glu Val  
 820 825 830  
 Ser Lys Leu Lys Asp Thr Arg Leu Leu Thr Phe Lys Ala Ile Ala Gln  
 835 840 845  
 35 Ile Phe Ile Leu Gly Cys Ser Trp Val Leu Gly Ile Phe Gln Ile Gly  
 850 855 860  
 40 Pro Leu Ala Ser Ile Met Ala Tyr Leu Phe Thr Ile Ile Asn Ser Leu  
 865 870 875 880  
 Gln Gly Ala Phe Ile Phe Leu Ile His Cys Leu Leu Asn Arg Gln Val  
 885 890 895  
 45 Arg Asp Glu Tyr Lys Lys Leu Leu Thr Arg Lys Thr Asp Leu Ser Ser  
 900 905 910  
 50 His Ser Gln Thr Ser Gly Ile Leu Leu Ser Ser Met Pro Ser Thr Ser  
 915 920 925  
 Lys Met Gly  
 930  
 55  
 <210> 7  
 <211> 740  
 <212> PRT

WO 01/18047

PCT/AU00/01083

14/19

&lt;213&gt; Homo sapiens

&lt;400&gt; 7

5	Met	Gly	Gly	Arg	Val	Phe	Leu	Ala	Phe	Cys	Val	Trp	Leu	Thr	Leu	Pro
	1				5					10					15	
	Gly	Ala	Glu	Thr	Gln	Asp	Ser	Arg	Gly	Cys	Ala	Arg	Val	Cys	Pro	Gln
			20						25					30		
10	Asn	Ser	Ser	Cys	Val	Asn	Ala	Thr	Ala	Cys	Arg	Cys	Asn	Pro	Gly	Phe
		35						40					45			
	Ser	Ser	Phe	Ser	Glu	Ile	Ile	Thr	Thr	Pro	Thr	Glu	Thr	Cys	Asp	Asp
		50					55					60				
15	Ile	Asn	Glu	Cys	Ala	Thr	Pro	Ser	Lys	Val	Ser	Cys	Gly	Lys	Phe	Ser
	65					70					75				80	
	Asp	Cys	Trp	Asn	Thr	Glu	Gly	Ser	Tyr	Asp	Cys	Val	Cys	Ser	Pro	Gly
20					85					90					95	
	Tyr	Glu	Pro	Val	Ser	Gly	Ala	Lys	Thr	Phe	Lys	Asn	Glu	Ser	Glu	Asn
			100						105					110		
25	Thr	Cys	Gln	Asp	Glu	Cys	Ser	Ser	Gly	Gln	His	Gln	Cys	Asp	Ser	Ser
			115					120					125			
	Thr	Val	Cys	Phe	Asn	Thr	Val	Gly	Ser	Tyr	Ser	Cys	Arg	Cys	Arg	Pro
		130					135					140				
30	Gly	Trp	Lys	Pro	Arg	His	Gly	Ile	Pro	Asn	Asn	Gln	Lys	Asp	Thr	Val
	145					150					155					160
	Cys	Glu	Asp	Met	Thr	Phe	Ser	Thr	Trp	Thr	Pro	Pro	Pro	Gly	Val	His
35					165					170					175	
	Ser	Gln	Thr	Leu	Ser	Arg	Phe	Phe	Asp	Lys	Val	Gln	Asp	Leu	Gly	Arg
				180					185					190		
40	Asp	Ser	Lys	Thr	Ser	Ser	Ala	Glu	Val	Thr	Ile	Gln	Asn	Val	Ile	Lys
			195					200					205			
	Leu	Val	Asp	Glu	Leu	Met	Glu	Ala	Pro	Gly	Asp	Val	Glu	Ala	Leu	Ala
		210					215					220				
45	Pro	Pro	Val	Arg	His	Leu	Ile	Ala	Thr	Gln	Leu	Leu	Ser	Asn	Leu	Glu
	225					230					235					240
	Asp	Ile	Met	Arg	Ile	Leu	Ala	Lys	Ser	Leu	Pro	Lys	Gly	Pro	Phe	Thr
50					245					250					255	
	Tyr	Ile	Ser	Pro	Ser	Asn	Thr	Glu	Leu	Thr	Leu	Met	Ile	Gln	Glu	Arg
			260					265						270		
55	Gly	Asp	Lys	Asn	Val	Thr	Met	Gly	Gln	Ser	Ser	Ala	Arg	Met	Lys	Leu
			275					280					285			
	Asn	Trp	Ala	Val	Ala	Ala	Gly	Ala	Glu	Asp	Pro	Gly	Pro	Ala	Val	Ala

WO 01/18047

PCT/AU00/01083

15/19

290 295 300  
Gly Ile Leu Ser Ile Gln Asn Met Thr Thr Leu Leu Ala Asn Ala Ser  
305 310 315 320  
5 Leu Asn Leu His Ser Lys Lys Gln Ala Glu Leu Glu Glu Ile Tyr Glu  
325 330 335  
10 Ser Ser Ile Arg Gly Val Gln Leu Arg Arg Leu Ser Ala Val Asn Ser  
340 345 350  
Ile Phe Leu Ser His Asn Asn Thr Lys Glu Leu Asn Ser Pro Ile Leu  
355 360 365  
15 Phe Ala Phe Ser His Leu Glu Ser Ser Asp Gly Glu Ala Gly Arg Asp  
370 375 380  
Pro Pro Ala Lys Asp Val Met Pro Gly Pro Arg Gln Glu Leu Leu Cys  
385 390 395 400  
20 Ala Phe Trp Lys Ser Asp Ser Asp Arg Gly Gly His Trp Ala Thr Glu  
405 410 415  
25 Val Cys Gln Val Leu Gly Ser Lys Asn Gly Ser Thr Thr Cys Gln Cys  
420 425 430  
Ser His Leu Ser Ser Phe Thr Ile Leu Met Ala His Tyr Asp Val Glu  
435 440 445  
30 Asp Trp Lys Leu Thr Leu Ile Thr Arg Val Gly Leu Ala Leu Ser Leu  
450 455 460  
Phe Cys Leu Leu Leu Cys Ile Leu Thr Phe Leu Leu Val Arg Pro Ile  
465 470 475 480  
35 Gln Gly Ser Arg Thr Thr Ile His Leu His Leu Cys Ile Cys Leu Phe  
485 490 495  
40 Val Gly Ser Thr Ile Phe Leu Ala Gly Ile Glu Asn Glu Gly Gly Gln  
500 505 510  
Val Gly Leu Arg Cys Arg Leu Val Ala Gly Leu Leu His Tyr Cys Phe  
515 520 525  
45 Leu Ala Ala Phe Cys Trp Met Ser Leu Glu Gly Leu Glu Leu Tyr Phe  
530 535 540  
Leu Val Val Arg Val Phe Gln Gly Gln Gly Leu Ser Thr Arg Trp Leu  
545 550 555 560  
50 Cys Leu Ile Gly Tyr Gly Val Pro Leu Leu Ile Val Gly Val Ser Ala  
565 570 575  
Ala Ile Tyr Ser Lys Gly Tyr Gly Arg Pro Arg Tyr Cys Trp Leu Asp  
580 585 590  
55 Phe Glu Gln Gly Phe Leu Trp Ser Phe Leu Gly Pro Val Thr Phe Ile  
595 600 605

WO 01/18047

PCT/AU00/01083

16/19

Ile Leu Cys Asn Ala Val Ile Phe Val Thr Thr Val Trp Lys Leu Thr  
 610 615 620  
 5 Gln Lys Phe Ser Glu Ile Asn Pro Asp Met Lys Lys Leu Lys Lys Ala  
 625 630 635 640  
 Arg Ala Leu Thr Ile Thr Ala Ile Ala Gln Leu Phe Leu Leu Gly Cys  
 645 650 655  
 10 Thr Trp Val Phe Gly Leu Phe Ile Phe Asp Asp Arg Ser Leu Val Leu  
 660 665 670  
 Thr Tyr Val Phe Thr Ile Leu Asn Cys Leu Gln Gly Ala Phe Leu Tyr  
 675 680 685  
 15 Leu Leu His Cys Leu Leu Asn Lys Lys Val Arg Glu Glu Tyr Arg Lys  
 690 695 700  
 20 Trp Ala Cys Leu Val Ala Gly Gly Ser Lys Tyr Ser Glu Phe Thr Ser  
 705 710 715 720  
 Thr Thr Ser Gly Thr Gly His Asn Gln Thr Arg Ala Leu Arg Ala Ser  
 725 730 735  
 25 Glu Ser Gly Ile  
 740  
 30 <210> 8  
 <211> 30  
 <212> DNA  
 <213> Artificial Sequence  
 35 <220>  
 <223> Description of Artificial Sequence: PCR primers  
 <400> 8  
 ctacggatcc aatatttcag cttcctgtcc 30  
 40  
 <210> 9  
 <211> 32  
 <212> DNA  
 45 <213> Artificial Sequence  
 <220>  
 <223> Description of Artificial Sequence: PCR primers  
 50 <400> 9  
 cgcgaagctt tcaatcttga catttctcat gg 32  
 55 <210> 10  
 <211> 34  
 <212> DNA  
 <213> Artificial Sequence



WO 01/18047

PCT/AU00/01083

17/19

<220>  
<223> Description of Artificial Sequence: PCR primers

5 <400> 10  
gacgggatcc aatgagtgtc tactgaaaga attg 34

10 <210> 11  
<211> 34  
<212> DNA  
<213> Artificial Sequence

15 <220>  
<223> Description of Artificial Sequence: PCR primers

<400> 11  
accgaagctt tcagctcttg ttcacataac aatc 34

20 <210> 12  
<211> 30  
<212> DNA  
<213> Artificial Sequence

25 <220>  
<223> Description of Artificial Sequence: PCR primers

30 <400> 12  
ctacggatcc aatatttcag ctctctgtcc 30

35 <210> 13  
<211> 34  
<212> DNA  
<213> Artificial Sequence

40 <220>  
<223> Description of Artificial Sequence: PCR primers

<400> 13  
accgaagctt tcagctcttg ttcacataac aatc 34

45 <210> 14  
<211> 31  
<212> DNA  
<213> Artificial Sequence

50 <220>  
<223> Description of Artificial Sequence: PCR primers

<400> 14  
acacggatcc actttgggag tactgagtga a 31

55 <210> 15  
<211> 32  
<212> DNA

WO 01/18047

PCT/AU00/01083

18/19

&lt;213&gt; Artificial Sequence.

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence: PCR primers

5

&lt;400&gt; 15

32

cgctaagctt tcatagagcc atgagcacag ca

10

&lt;210&gt; 16

&lt;211&gt; 20

&lt;212&gt; DNA

&lt;213&gt; Mus musculus

15

&lt;400&gt; 16

20

cacctgcagc tcttccatct

20

&lt;210&gt; 17

&lt;211&gt; 23

&lt;212&gt; DNA

&lt;213&gt; Mus musculus

25

&lt;400&gt; 17

23

gaaagtttgc ttctcaaaat cca

30

&lt;210&gt; 18

&lt;211&gt; 26

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

35

&lt;400&gt; 18

26

tgtctcattg cacctcttgg ttccat

40

&lt;210&gt; 19

&lt;211&gt; 19

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

45

&lt;400&gt; 19

19

ccacaacagc acccactgt

50

&lt;210&gt; 20

&lt;211&gt; 33

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

55

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence: PCR primer

&lt;400&gt; 20

33

tagtagacgc gtatattaca aatgatgaat att

&lt;210&gt; 21

WO 01/18047

PCT/AU00/01083

19/19

<211> 33  
<212> DNA  
<213> Artificial Sequence

5 <220>  
<223> Description of Artificial Sequence: PCR primer

<400> 21  
tagtagacgc gttcaatcac taatagttct gct 33

10

<210> 22  
<211> 26  
<212> DNA  
15 <213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PCR primer

20 <400> 22  
cgggatactc ctcattgggt agagcc 26

<210> 23  
<211> 33  
<212> DNA  
25 <213> Artificial Sequence

<220>  
30 <223> Description of Artificial Sequence: PCR primer

<400> 23  
cgggtaccac catgggaagc aggtgccttc tgc 33

35

<210> 24  
<211> 24  
<212> DNA  
40 <213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PCR primer

<400> 24  
45 ggaaytagaa caccaggttt atca 24

<210> 25  
<211> 18  
<212> DNA  
50 <213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PCR primer

55 <400> 25  
cctcttctcg gccacac 18